

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/763,331

DATE: 07/11/2001

TIME: 11:25:16

Input Set : A:\PTO.txt

Output Set: N:\CRF3\07112001\I763331.raw

ENTERED

4 <110> APPLICANT: Martin, Charles E.
 5 Mitchell, Andrew
 8 <120> TITLE OF INVENTION: Synthetic Fatty Acid Desaturase Gene for
 9 Expression in Plants
 12 <130> FILE REFERENCE: 97-0081 PCT
 C--> 14 <140> CURRENT APPLICATION NUMBER: US/09/763,331
 C--> 14 <141> CURRENT FILING DATE: 1999-08-24
 14 <150> PRIOR APPLICATION NUMBER: US 60/097,586
 15 <151> PRIOR FILING DATE: 1998-08-24
 17 <160> NUMBER OF SEQ ID NOS: 8
 19 <170> SOFTWARE: FastSEQ for Windows Version 4.0
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 22 <211> LENGTH: 1555
 23 <212> TYPE: DNA
 24 <213> ORGANISM: Saccharomyces cerevisiae
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 28 ggatgactct gccagcagtg gcattgtcga cgaagtcgac ttaacggaag ctaatatattt 120
 29 ggctactggt ttgaataaga aagcaccaag aattgtcaac gggttttggtt ctttaattggg 180
 30 ctccaaggaa atgggtttccg tggaaattcga caagaaggga aacgaaaaga agtccaattt 240
 31 ggatcgtctg ctagaaaagg acaaccaaga aaaagaagaa gctaaaacta aaattcacat 300
 32 ctccgaacaa ccatggactt tgaataactg gcaccaacat ttgaactggt tgaacatggt 360
 33 tcttgtttgt ggtatgcaa tgattggttg gtacttcgct ctctctggta agtaccttt 420
 34 gcatttaaac gttttccttt tctccgtttt ctactacgct gtcggtggtg tttctattac 480
 35 tgccggttac catagattat ggtctcacag atcttactcc gctcactggc cattgagatt 540
 36 attctacgct atcttcggtt gtgcttccgt tgaagggtcc gctaaatggt ggggccactc 600
 37 tcacagaatt caccatcgtt acactgatac cttgagagat ctttatgacg ctctagagag 660
 38 tctatggtac tcccacatgg gatggatgct tttgaagcca aatccaaaat acaaggctag 720
 39 agctgatatt accgatatga ctgatgattg gaccattaga ttccaacaca gacactacat 780
 40 cttgttgatg ttattaaccg ctttcgtcat tccaactctt atctgtggtt actttttcaa 840
 41 cgactatatg ggtggtttga tctatgccgg ttttattcgt gtctttgtca ttcaacaagc 900
 42 taccttttgc attaaactca tggctcatta catcggtacc caaccattcg atgacagaag 960
 43 aaccctcgt gacaactgga ttactgcat tgttactttc ggtgaagggt accataactt 1020
 44 ccaccacgaa ttcccaactg attacagaaa cgctattaag tggtagcaat acgacccaac 1080
 45 taagggtatc atctatttga cttctttagt tggcttagca tacgacttga agaaattctc 1140
 46 tcaaaatgct attgaagaag ccttgattca acaagaacaa aagaagatca ataaaaagaa 1200
 47 ggctaagatt aactggggtc cagttttgac tgatttgcca atgtgggaca acaaaacctt 1260
 48 cttggctaag tctaaggaaa acaagggttt ggttatcatt tctggtattg ttcacgacgt 1320
 49 atctggttat atctctgaac atccaggtgg tgaaacttta attaaaactg cattaggtaa 1380
 50 ggacgctacc aaggctttca gtggtggtgt ctaccgtcac tcaaatgccg ctcaaatgt 1440
 51 cttggctgat atgagagtgg ctgttatcaa ggaaagtaag aactctgcta ttagaatggc 1500
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 54 <210> SEQ ID NO: 2
 55 <211> LENGTH: 510
 56 <212> TYPE: PRT
 57 <213> ORGANISM: Saccharomyces cerevisiae
 59 <400> SEQUENCE: 2

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60 Met Pro Thr Ser Gly Thr Thr Ile Glu Leu Ile Asp Asp Gln Phe Pro
61 1 5 10 15
62 Lys Asp Asp Ser Ala Ser Ser Gly Ile Val Asp Glu Val Asp Leu Thr
63 20 25 30
64 Glu Ala Asn Ile Leu Ala Thr Gly Leu Asn Lys Lys Ala Pro Arg Ile
65 35 40 45
66 Val Asn Gly Phe Gly Ser Leu Met Gly Ser Lys Glu Met Val Ser Val
67 50 55 60
68 Glu Phe Asp Lys Lys Gly Asn Glu Lys Lys Ser Asn Leu Asp Arg Leu
69 65 70 75 80
70 Leu Glu Lys Asp Asn Gln Glu Lys Glu Glu Ala Lys Thr Lys Ile His
71 85 90 95
72 Ile Ser Glu Gln Pro Trp Thr Leu Asn Asn Trp His Gln His Leu Asn
73 100 105 110
74 Trp Leu Asn Met Val Leu Val Cys Gly Met Pro Met Ile Gly Trp Tyr
75 115 120 125
76 Phe Ala Leu Ser Gly Lys Val Pro Leu His Leu Asn Val Phe Leu Phe
77 130 135 140
78 Ser Val Phe Tyr Tyr Ala Val Gly Gly Val Ser Ile Thr Ala Gly Tyr
79 145 150 155 160
80 His Arg Leu Trp Ser His Arg Ser Tyr Ser Ala His Trp Pro Leu Arg
81 165 170 175
82 Leu Phe Tyr Ala Ile Phe Gly Cys Ala Ser Val Glu Gly Ser Ala Lys
83 180 185 190
84 Trp Trp Gly His Ser His Arg Ile His His Arg Tyr Thr Asp Thr Leu
85 195 200 205
86 Arg Asp Pro Tyr Asp Ala Arg Arg Gly Leu Trp Tyr Ser His Met Gly
87 210 215 220
88 Trp Met Leu Leu Lys Pro Asn Pro Lys Tyr Lys Ala Arg Ala Asp Ile
89 225 230 235 240
90 Thr Asp Met Thr Asp Asp Trp Thr Ile Arg Phe Gln His Arg His Tyr
91 245 250 255
92 Ile Leu Leu Met Leu Leu Thr Ala Phe Val Ile Pro Thr Leu Ile Cys
93 260 265 270
94 Gly Tyr Phe Phe Asn Asp Tyr Met Gly Gly Leu Ile Tyr Ala Gly Phe
95 275 280 285
96 Ile Arg Val Phe Val Ile Gln Gln Ala Thr Phe Cys Ile Asn Ser Leu
97 290 295 300
98 Ala His Tyr Ile Gly Thr Gln Pro Phe Asp Asp Arg Arg Thr Pro Arg
99 305 310 315 320
100 Asp Asn Trp Ile Thr Ala Ile Val Thr Phe Gly Glu Gly Tyr His Asn
101 325 330 335
102 Phe His His Glu Phe Pro Thr Asp Tyr Arg Asn Ala Ile Lys Trp Tyr
103 340 345 350
104 Gln Tyr Asp Pro Thr Lys Val Ile Ile Tyr Leu Thr Ser Leu Val Gly
105 355 360 365
106 Leu Ala Tyr Asp Leu Lys Lys Phe Ser Gln Asn Ala Ile Glu Glu Ala
107 370 375 380
108 Leu Ile Gln Gln Glu Gln Lys Lys Ile Asn Lys Lys Lys Ala Lys Ile

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109 385          390          395          400
110 Asn Trp Gly Pro Val Leu Thr Asp Leu Pro Met Trp Asp Lys Gln Thr
111          405          410          415
112 Phe Leu Ala Lys Ser Lys Glu Asn Lys Gly Leu Val Ile Ile Ser Gly
113          420          425          430
114 Ile Val His Asp Val Ser Gly Tyr Ile Ser Glu His Pro Gly Gly Glu
115          435          440          445
116 Thr Leu Ile Lys Thr Ala Leu Gly Lys Asp Ala Thr Lys Ala Phe Ser
117          450          455          460
118 Gly Gly Val Tyr Arg His Ser Asn Ala Ala Gln Asn Val Leu Ala Asp
119 465          470          475          480
120 Met Arg Val Ala Val Ile Lys Glu Ser Lys Asn Ser Ala Ile Arg Met
121          485          490          495
122 Ala Ser Lys Arg Gly Glu Ile Tyr Glu Thr Gly Lys Phe Phe
123          500          505          510
126 <210> SEQ ID NO: 3
127 <211> LENGTH: 1555
128 <212> TYPE: DNA
129 <213> ORGANISM: Artificial Sequence
131 <220> FEATURE:
132 <223> OTHER INFORMATION: synthetic yeast delta-9 desaturase gene modified
133 for expression in plants
135 <400> SEQUENCE: 3
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137 ggatgattct gcttcttctg gaatcgttga tgaggttgat cttactgagg ctaacatcct      120
138 tgctactgga cttacaaga aggctcctag aatcgttaac ggattcggat ctcttatggg      180
139 atctaaggag atggtttctg ttgagttcga taagaaggga aacgagaaga agtctaacct      240
140 tgatagactt cttgagaagg ataaccaaga gaaggaggag gctaagacta agatccatat      300
141 ctctgagcaa ccttggactc tcaacaactg gcatcaacat ctcaactggc tcaacatggt      360
142 gctcgtctgt ggaatgccta tgatcggatg gtacttcgct ctctctggaa aagtgcctct      420
143 ccatctcaac gttttcctct tctctgtcct ctactacgct gttggaggag tgtctatcac      480
144 tgctggatac catagactct ggtctcatag atcttactct gctcattggc ctcttagact      540
145 cttctacgct atctttggat gtgcttctgt tgagggatct gctaagtggg ggggacattc      600
146 tcatagaatc catcatagat aactgatac tcttagagat ccttacgatg ctagaagagg      660
147 actttggtac tctcatatgg gatggatgct tcttaagcct aaccctaagt acaaggctag      720
148 agctgatatc actgatatga ctgatgattg gactatcaga ttccaacata gacattacat      780
149 cttgctcatg ctcccttactg ctttcgtgat ccctactctc atctgtggat acttcttcaa      840
150 cgattacatg ggaggactca tctacgctgg attcatcaga gtgttcgtca tccaacaagc      900
151 tactttctgt atcaactcta tggctcatta catcggaact caacctttcg atgatagaag      960
152 aactcctaga gataactgga tcaactgctat cgttactttc ggagagggat accataactt      1020
153 ccatcatgag ttccctactg attatagaaa cgctatcaag tggtaaccaat acgatcctac      1080
154 taaagtgatc atctacttga cttctctcgt gggacttgct tacgatctca agaagttctc      1140
155 tcaaaacgct atcgaggagg ctcttatcca acaagagcaa aagaagatca acaagaagaa      1200
156 ggctaagatt aattggggac ctgttcttac tgatcttcct atgtgggata agcaaaacttt      1260
157 ccttgctaag tctaaggaga acaagggact tgttatcatc tctggaatcg ttcgatgatg      1320
158 ttctggatac atctctgagc atcctggagg agagacttta attaagactg ctcttggaag      1380
159 ggatgctact aaggccttct ctggaggagt ttacagacat tctaacgctg ctcaaaacgt      1440
160 gcttgctgat atgagagttg ctgttatcaa ggagtctaag aactctgcta tcagaatggc      1500
161 ttctaagaga ggagagatct acgagactgg aaagttcttc tgatctagag gatcc      1555

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163 <210> SEQ ID NO: 4
164 <211> LENGTH: 383
165 <212> TYPE: PRT
166 <213> ORGANISM: Arabidopsis thaliana
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172 20 25 30
173 Val Gly Asp Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser
174 35 40 45
175 Ile Pro Arg Ser Phe Ser Tyr Leu Ile Ser Asp Ile Ile Ile Ala Ser
176 50 55 60
177 Cys Phe Tyr Tyr Val Ala Thr Asn Tyr Phe Ser Leu Leu Pro Gln Pro
178 65 70 75 80
179 Leu Ser Tyr Leu Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val
180 85 90 95
181 Leu Thr Gly Ile Trp Val Ile Ala His Glu Cys Gly His His Ala Phe
182 100 105 110
183 Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser
184 115 120 125
185 Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg His
186 130 135 140
187 His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys
188 145 150 155 160
189 Gln Lys Ser Ala Ile Lys Trp Tyr Gly Lys Tyr Leu Asn Asn Pro Leu
190 165 170 175
191 Gly Arg Ile Met Met Leu Thr Val Gln Phe Val Leu Gly Trp Pro Leu
192 180 185 190
193 Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Phe Ala Cys
194 195 200 205
195 His Phe Phe Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu Gln
196 210 215 220
197 Ile Tyr Leu Ser Asp Ala Gly Ile Leu Ala Val Cys Phe Gly Leu Tyr
198 225 230 235 240
199 Arg Tyr Ala Ala Ala Gln Gly Met Ala Ser Met Ile Cys Leu Tyr Gly
200 245 250 255
201 Val Pro Leu Leu Ile Val Asn Ala Phe Leu Val Leu Ile Thr Tyr Leu
202 260 265 270
203 Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp Asp
204 275 280 285
205 Trp Leu Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile Leu
206 290 295 300
207 Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His Leu
208 305 310 315 320
209 Phe Ser Thr Met Pro His Tyr Asn Ala Met Glu Ala Thr Lys Ala Ile
210 325 330 335
211 Lys Pro Ile Leu Gly Asp Tyr Tyr Gln Phe Asp Gly Thr Pro Trp Tyr
212 340 345 350

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214          355          360          365
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220 <211> LENGTH: 1372
221 <212> TYPE: DNA
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227 ctacttcttc caagaaatcg gaaaccgaca ccacaaagcg tgtgccgtgc gagaaaccgc      180
228 ctttctcggg gggagatctg aagaaagcaa tcccgccgca ttgtttcaaa cgctcaatcc      240
229 ctctgtcttt ctctacatt atcagtgcac tcattatagc ctcatgcttc tactacgtcg      300
230 ccaccaatta ctctctctc ctccctcagc ctctctctta cttggcttgg ccactctatt      360
231 gggcctgtca aggctgtgtc ctaactggta tctgggtcat agcccacgaa tgcggtcacc      420
232 acgcattcag cgactaccaa tggctggatg acacagtggg tcttatcttc cattccttcc      480
233 tcctcgtccc ttacttctcc tggaaagata gtcacgcccg tcaccattcc aacactggat      540
234 ccctcgaaag agatgaagta tttgtcccaa agcagaaatc agcaatcaag tggtagcgga      600
235 aatacctcaa caaccctctt ggacgcacat tgatgttaac cgtccagttt gtcctcgggt      660
236 ggcccttgta cttagccttt aacgtctctg gcagaccgta tgacgggttc gcttgccatt      720
237 tcttccccaa cgctcccatc tacaatgacc gagaacgcct ccagatatac ctctctgatg      780
238 cgggtattct agccgtctgt tttggtcttt accgttacgc tgctgcacaa gggatggcct      840
239 cgatgatctg cctctacgga gtaccgcttc tgatagtga tgcgttcctc gtcttgatca      900
240 cttacttgca gcacactcat ccctcgttgc ctactacga ttcacacag tgggactggc      960
241 tcaggggagc tttggctacc gtacacagag actacggaat cttgaacaag gtgttccaca      1020
242 acattacaga cacacacgtg gctcatcacc tgttctcgac aatgccgcat tataacgcaa      1080
243 tggaaagctac aaaggcgata aagccaattc tgggagacta ttaccagttc gatggaacac      1140
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245 aagggtgacaa gaaagggtgt tactggtaca acaataagtt atgagcatga tggatgaagaa      1260
246 attgtcgacc tttctcttgt ctgtttgtct tttgttaaag aagctatgct tcgttttaaat      1320
247 aatcttattg tccattttgt tgtgttatga cattttggct gtcattatg tt      1372
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255 <211> LENGTH: 33
256 <212> TYPE: PRT
257 <213> ORGANISM: Arabidopsis thaliana
259 <400> SEQUENCE: 7
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262 Pro Asp Arg Glu Gly Asp Lys Lys Gly Val Tyr Trp Tyr Asn Asn Lys
263          20          25          30
264 Leu
268 <210> SEQ ID NO: 8
269 <211> LENGTH: 30
270 <212> TYPE: PRT
271 <213> ORGANISM: Saccharomyces cerevisiae

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VERIFICATION SUMMARY

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L:14 M:270 C: Current Application Number differs, Replaced Current Application No

L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:252 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (6) SEQUENCE:

I763331.05331